D1 cont.d

either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment of (d)(2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric genes results in an altered corn oil phenotype.

Remarks

Claims 172-176 have been amended to address the rejections under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The term "complement" has been substituted for the term "reverse complement." Support for this substitution can be found in the specification on page 16 at lines 29-35. Thus, no new matter has been added.

The term "or a functionally equivalent subfragment thereof" has been clarified to refer to the nucleic acid in the chimeric gene.

Claims 172-172, sections (ii) and (iv) have been clarified to recite the nucleic acid to which is referred in the claim. Also, the language around "corn oleosin promoter hybridizes to the" has been also been clarified. No new matter has been added.

In view of the foregoing, withdrawal of the rejection under 35 USC §112, second paragraph, is respectfully requested.

Concern over the term "carcass quality improving amount" was raised as being indefinite under 35 USC §112, second paragraph. In view of the below discussion and information submitted herewith it is respectfully submitted that this concern is not warranted.

Claims 172-176 were rejected under 35 USC §112, second paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. References were cited on page 4 of the Office Action "to demonstrate that it is highly unpredictable as to how feeding regimes will effect the carcass quality of animals."

It is further stated on page 5 of the Office Action that due "to the broad nature of the claims, the lack of guidance in the specification or in the prior art, the high level of unpredictability with regard to the effects of feeding regimes on animal carcass quality, the lack of working examples, and the high level of experimentation necessary to determine the methodology necessary to practice the claimed invention, it is concluded that undue experimentation would be required to practice the claimed invention."

Submitted herewith is a copy of an index from the Optimum® High Oil Corn Technical Information and copies of a number of the articles mentioned therein. Also included are copies of some articles from Nutritional Insights which appears on the Pioneer Hi-Bred International, Inc. web site and a copy of a May/June 1999 article from Feed Lot, Vol. VII, No. 3, appearing on its website regarding the use of Optimum High Oil Corn to improve performance and carcass quality, specifically, in cattle beef.

The Nutritional Insights article entitled "Benefits of Feeding Optimum® High Oil Corn To Finishing Beef Cattle Research Studies to Determine Feeding Value (Summary) indicates that Optimum® High Oil Corn can effectively replace 100% of typical corn and up to 3% added fat in finishing beef cattle diets. Cattle fed with this high oil corn, according to the studies, generally produced carcasses having a higher % choice or better than those fed typical corn without added fat.

Copies of the articles discussing the Colorado study, Idaho Study and the Iowa Study are included herewith.

The articles describe the feeding trials and how they were conducted. Carcass quality data is presented on page 2.

The University of Idaho feeding trial demonstrated that feeding high oil corn improved the marbling scores and carcass quality grades of finishing beef steers compared to those fed typical corn. The conditions for the feeding trial are set forth on the first page and Carcass Quality data is set forth in Table 5. It is stated on page 1 that the "Idaho trial used 60 head of yearling Angus-cross steers that averaged 906 pounds and were fed in an 84-day finishing trial. Three treatments of 20 head each were evaluated as: 1) control (typical corn), 2) high oil corn, and 3) high oil corn fed at a level isocaloric to control (increased roughage level). All corn was dry rolled and fed in a total mixed ration. The rations were iso-nitrogenous by adjusting the urea level in the diet. The high oil corn averaged 7.04% while the normal corn averaged 4.86% oil on a dry matter basis. Steers were fed to appetite twice daily using

individual electronic gates and were implanted with Synovex-SO at the start of the trial. . . ."

The Iowa study reported that there "were no effects of feeding high oil corn on carcass characteristics, except there were more choice carcasses from the steers fed high oil corn as compared with the control."

The Dupont Specialty Grains articles present feeding trials involving pork, beef and poultry. The feeding regimens are set forth and are fairly detailed. The studies took place in the 1991-1999 time frame.

Five additional references are included to demonstrate that feeding studies involving pigs show a clear, reproducible, and rapid alteration of carcass quality when oil compositions of the feed are modified (Whittington et al. (1986) *J.Sci.Food Agric. 37*:753-761; Myer et al. (1992) *J.Anim.Sci. 70*:3734-3741; Hansen (2001) *Proceedings of the Carolina Nutrition Conference*. Raleigh, NC; Madsen et al. (1992) *Anim. Sci. 42*:220-225; and Gatlin et al. (2002) *J. Anim. Sci. 80*:1606-1615). Applicants have selected these five publications as a representative sample of 29 publications that can be made available to the examiner if additional information is required.

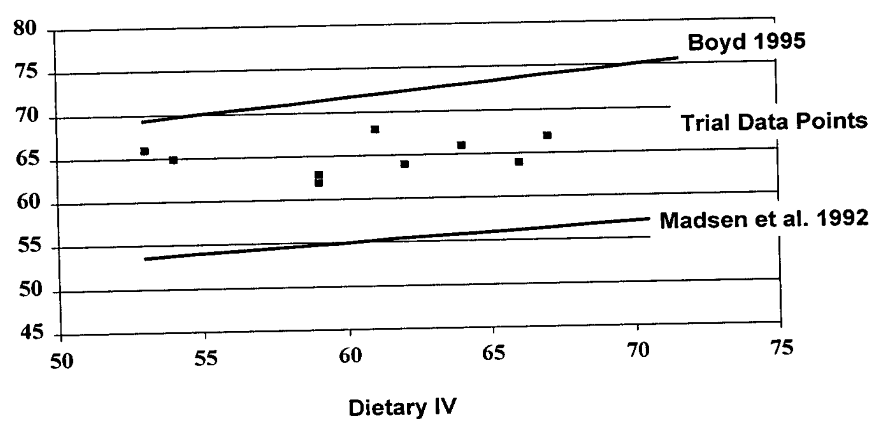
Whittington et al. conclude that lowering the amount of linoleic acid, an 18:2 polyunsaturated fatty acid, in the feed results in a lowering of polyunsaturated fatty acids (PUFAs) in the fat of the pigs. This improves the carcass quality of the animals by increasing the firmness of the pork fat. Myer et al. concluded that pigs fed a high oleic (18:1 monounsaturated fatty acid) diet , that was low in PUFAs, resulted in carcasses with increased saturated fat and lower PUFAs. Hansen concludes that dietary fat is the primary factor in swine feed that determines carcass quality characteristics. Furthermore, short-term feeding that results in carcass quality change is tightly linked to fat type or level of the feed. Hansen claims that these types of results are clear and predictable. Madsen et al. review the relationship of oil composition in pig feed to various parameters of carcass quality. The general conclusion, relevant to the present invention, is that high levels of PUFAs increases fat softness (an undesirable trait) and shortens shelf-life (the fat goes rancid faster than more saturated fat). Gatlin et al. further refine the composition of the feed to increase mono-unsaturated and lower PUFAs, which results in improved fat firmness in as little as 6-8 weeks of feeding.

Clearly the information set forth in these articles shows that those skilled in the art know how to adjust feeding regimens and that to the extent any experimentation is needed it is not undue. The wealth of information presented in these articles shows how different animals are fed, what they

are fed, how the diets are adjusted and how the improvement in carcass quality is assessed.

It is possible to show that dietary fat and pork carcass quality are related by plotting the iodine values (IV, an indicator of the degree of fat saturation or hardness) of pork fat taken from animals fed varying dietary feed compositions. Data presented in the Madsen reference (pork IV – 47.1 + (0.14 x IVP))and data from a separate study (Boyd (1995) "Effect of dietary linoleic acid intake on body fat deposition of linoleic acid in growing pigs" PIC USA Franklin, KY; pork IV = 52.4 + (0.315 x IVP)) were plotted below and both show a clear correlation between dietary fat and pork carcass quality. The fact that the two unrelated studies both show approximately parallel responses is taken as further evidence that feeding and resulting carcass quality are reproducible phenomena. Trial data points on the graph below represent combined results from feeding studies of Trial COSW11200100 (typical corn, 60% high oleic corn, and combinations of corn oil and high oleic sunflower oil were used to simulate the transgenic corn oil composition) and Trial COSW01SWG003 (typical corn, 60% high oleic corn and 80% high oleic soybeans fed individually and in combination). These results are consistent with previous results and demonstrate that high oleic corn would be expected to improve the carcass quality of feed animals.

Relationship between dietary IV and pork carcass IV



Regarding Machev et al. which is described on page 4 of the Office Action as disclosing that "completely replacing maize with barley in animal feed had no significant effect on the slaughter and commercial value of pigs

(ABSTRACT, p.26). . . .", it is noted that this article does not appear to disclose the composition of the "grower mixture" and "finisher mixture" used in the feeding studies except to say that grain is 74% and 80% (respectively) of the feed. It is not clear what constituted the remainder of the feed. Given this, it is not appropriate to conclude anything since the unknown components may have contributed to the overall outcome. It is possible that if one of ordinary skill in the art was aware of all of the composition of the feed it may have been understandable as to how the feeding regimen affected carcass quality.

In addition, the examiner states that the replacement of barley for corn in the animal feed of the Machev article would be expected to have a greater effect on carcass quality than the replacement of high-oleic corn (of the present invention) for wild-type corn. As shown in the table below the composition of high oleic corn to typical corn is significantly different from both typical corn and barley, particularly with respect to PUFA content, which as stated above, has a demonstrable effect on lowering carcass quality. This is further shown by the iodine value, which is an indicator of oil saturation or hardness. Therefore, it is believed that one would expect a greater effect on carcass quality from substituting the grain of the present invention than replacing corn with barley.

% Fatty Acid	Barley[1]	Typical Corn[2]	High Oleic Corn[3]
Palmitic	21-29	11	4
Stearic	0.6-1.8	2	5
Oleic	10-16	24	81
Linoleic	52-58	62	9
Linolenic	5-7	1	1
Saturated	22-31	13	9
Mono-unsaturated	10-16	24	81
PUFA	57-65	64	10
Iodine Value	122	131	88

[1]Welch, R.W. 1979. Genotypic variation in oil and protein in barley grain. J. Sci Food and Agric. 29:953-958
[2]Corn: Chemistry and Technology. American Association of Cereal Chemists. 1987
[3]Expected fatty acid composition of transgenic high oleic corn grain

Thus, it is respectfully submitted that the determination of such factors does not involve undue experimentation and is well within the ordinary level of skill in the art at the time the invention was made.

Furthermore, claims 172-176 were rejected under 35 USC §112, second paragraph, on the ground that the plants described for use as animal feed, that the specification does not "reasonably provide enablement for the claimed plants."

As was noted in the previous response, the Examiner's attention is kindly invited to Example 8 in the specification which describes (1) transgenic corn with high saturate fatty acid composition in the grain, (2) transgenic corn with a high oleic acid content in the grain and (3) transgenic corn with high levels of saturated and oleic acid in kernels. The specification and examples show one of ordinary skill in the art how to the practice the claimed invention.

Given that the instant application concerns the use of isolated nucleic acid fragments encoding corn delta-12 and delta-9 desaturase in chimeric gene constructs with strong embryo-specific promoters to produce high oleic corn varieties, submitted herewith are copies of U.S. Patent Nos. 6,372,965, 5,443,974, 5,760,206 and 5,952,544 which further demonstrate success by Applicants' assignee in making plants with altered lipid content, e.g. high oleic seed content.

Elevation of the fraction of fatty acid moieties in seed oil that are oleic acid is accomplished primarily by blocking the activity of the endoplasmic reticulum form of delta-12 desaturase ('965 patent), the activity that would introduce a second site of unsaturation in the acid chain. Secondary enhancement of the elevation of oleate in oils may be achieved by simultaneously suppressing the activity of delta-15 desaturase ('544 patent) or overexpressing delta-9 desaturase ('974 and '206 patents).

It is respectfully submitted in view of the disclosure in the specification and the attached submissions that one of ordinary skill in the art would be able to work with these disclosures in producing plants/seeds having the claimed oil profiles.

Claims 172-176 were rejected under 35 USC §112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s) at the time the application was filed, had possession of the claimed invention.

It is respectfully submitted that in view of the information presented in the specification coupled the above discussion concerning the previous successes of Applicants' assignee in altering the oil profiles of plants as demonstrated by U.S. Patent Nos. 6,372,965 (WO 94/11516 published

May 26, 1994), 5,443,974, 5,760,206 and 5,952,544 that the written description does indeed demonstrate possession of the claimed invention.

It is believed that the section of the Office Action entitled "Response to Remarks" is addressed by the above clarifications to the claims and above dicusssion. With respect to the comment made on page 13 of the Office Action that "the claims embrace the use of nucleic acids that are not properly described with a structure-function relationship. . . .", it is respectfully submitted that the claims indeed recite structure (sequence identity of at least 80% based on the Clustal method of alignment) and correlate it with function either a corn delta-12 desaturase or a corn delta-9 stearoyl ACP desaturase or reference is made to corn oleosin promoter.

In view of the above discussion, references attached hereto and claim clarifications, withdrawal of the rejection of the claims is respectfully requested.

A version with markings to show changes made also accompanies this response.

A petition for a three (3) month extension of time and a petition to file a notice of appeal also accompanies this response.

The following documents are also attached:

- DuPont Specialty Grains, OPTIMUM® High Oil Corn Technical Information
- Pioneer, Benefits of Feeding OPTIMUM* High Oil Corn To Finishing Beef Cattle Introduction/Nutritional Considerations
- Pioneer, Benefits of Feeding High Oil Corn To Finishing Beef Cattle Research Studies to Determine Feeding Value (Colorado Study)
- Pioneer, Benefits of Feeding High Oil corn To Finishing Beef Cattle Research Studies to Determine Feeding Value (Idaho Study)
- Pioneer, Benefits of Feeding High Oil Corn To Finishing Beef Cattle Research Studies to Determine Feeding Value (Iowa State Study)
- Pioneer, Benefits of Feeding High Oil Corn To Finishing Beef Cattle Research Studies to Determine Feeding Value (Summary)
- Feed Lot™ Optimum High Oil corn Improves Performance and Carcass Quality
-
- DuPont Specialty Grains, Effect of OPTIMUM® High Oil Corn on Performance and Carcass Characteristics of Finishing Yearling Steers
- DuPont Specialty Grains, Feedlot Performance, Carcass Merit, and Profitability of Finishing Steers Fed Steam-flaked OPTIMUM® High Oil Corn Compared with Those Fed Steam-flaked Typical Corn plus 3% Added Tallow
- DuPont Specialty Grains, Effect of OPTIMUM® High Oil Corn on the Performance and Carcass Characteristics of Finishing Steers

- DuPont Specialty Grains, Effects of Combinations of Dry Rolled OPTIMUM® High Oil Corn and High Starch Corn on Performance of Finishing Feedlot Steers
- DuPont Specialty Grains, Effect of OPTIMUM® High Oil Corn or Added Dietary Fat on Pig Growth Performance and Meat Quality
- DuPont Specialty Grains, Growth Performance, Carcass Characteristics and Pork Quality of Pigs Fed Typical Corn Plus Fat or OPTIMUM® High Oil Corn
- DuPont Specialty Grains, Effect of OPTIMUM® High Oil Corn on Pig Growth and Carcass Characteristics
- A. Madsen et al., Influence of Dietary Fat on Carcass Fat Quality in Pigs. A Review
- F. Whittington et al., The Effect of Dietary Linoleic Acid on the Firmness of Backfat in Pigs of 85 kg. Live Weight
- L. A. Gatlin et al., The Effects of Dietary Fat Sources, Levels, and Feeding Intervals on Pork Fatty Acid Composition
- R. O. Myer et al., Dffect of Feeding High-Oleic-Acid Peanuts to Growing –Finishing Swine on Resulting Carcass fatty Acid Profile and on Carcass and Meat Quality Characteristics
- J. A. Hansen et al., Dietary Influencers of Pork Quality and Practical Solutions to Quality Problems
- Collins et al., Effect of Feeding OPTIMUM® High Oil Corn on Pellet Quality, Broiler Performance and Carcass Traits
- DuPont Specialty Grains, OPTIMUM® High Oil Corn: An Evaluation of its Nutritional Value in BUTA Tom and Hen Turkeys
- DuPont Specialty Grains, Nutritional Value of OPTIMUM® High Oil Corn in Nicholas Tom Turkeys
- DuPont Specialty Grains, OPTIMUM® Research Report Utility of OPTIMUM® High Oil Corn Grain for Commercial Turkeys (Summary of Four Research Reports)

It is respectfully submitted that this case is in form for allowance which allowance is respectfully requested.

Please charge any requisite fees or credits in connection with the filing of this Response After Final to Deposit Account No. 04-1928 (E. I. Du Pont de Nemours and Company).

Respectfully submitted,

Lynne M. Christenbury

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Dated: August 23, 2002

Version with Markings to Show Changes Made

In showing the changes, deleted material is bracketed, and inserted material is underlined.

In the Claims

Kindly amend Claims 172-176 as follows:

172. (twice amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u> , or the [reverse] complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] <u>of (ii)(b)</u> hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from

SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the [reverse] complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the [reverse] complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (iv) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

173. (twice amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-12 desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] <u>of (ii) (b)</u> hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-12 desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-12 desaturase</u>, or the [reverse] complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] <u>of (iv) (b)</u> hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1

intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

174. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-12 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-12 desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and (c) an isolated nucleic

acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (ii) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences,

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the [reverse] complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or the [reverse] complement thereof, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or the [reverse] complement thereof, (c) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the

isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (iv)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, and (d) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric gene results in an altered corn oil phenotype.

175. (twice amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of a corn grain obtained from a corn plant or plant part which comprises a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1, 58 or 59, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences;

wherein expresssion of the chimeric gene results in an altered corn oleic acid phenotype, and

further wherein the corn grain has an oil content in the range from about 6% to about 10% on a dry matter basis and further wherein said oil is comprised of not less than 60% oleic acid of the total oil content of the seed.

176. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase

has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] <u>of (b) (2) (A)</u> hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment [thereof] <u>of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase</u>, or the [reverse] complement of either the fragment or

subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (d)(2)(A) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (b) (2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a

functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the [reverse] complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment [thereof] of the isolated nucleic acid fragment encoding a corn delta-12 stearoyl ACP desaturase, or the [reverse] complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment [comprising a full length or partial corn oleosin promoter] of (d)(2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric genes results in an altered corn oil phenotype.